RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/543,122
Source: PCT
Date Processed by STIC: 6/14/06

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RAW SEQUENCE LISTING DATE: 06/14/2006
PATENT APPLICATION: **US/10/543,122** TIME: 10:29:10

Input Set : **A:\186563-US-2.ST25.txt**
Output Set: **N:\CRF4\06142006\J543122.raw**

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      3 <110> APPLICANT: Shenoy, Sudha
      4       Lefkowitz, Robert J.
      6 <120> TITLE OF INVENTION: Modified Trafficking Patterns for Arrestin and G-Protein-
Coupled
      7       Receptors via Arrestin-Ubiquitin Chimera
      9 <130> FILE REFERENCE: 186563/US/2 (469390-00352)
     11 <140> CURRENT APPLICATION NUMBER: US 10/543,122
C--> 12 <141> CURRENT FILING DATE: 2005-07-21
     14 <150> PRIOR APPLICATION NUMBER: US 60/442,403
     16 <151> PRIOR FILING DATE: 2003-01-24
     17 <160> NUMBER OF SEQ ID NOS: 45
     19 <170> SOFTWARE: PatentIn version 3.3
     21 <210> SEQ ID NO: 1
     22 <211> LENGTH: 1581
     23 <212> TYPE: DNA
     24 <213> ORGANISM: Artificial
     26 <220> FEATURE:
     27 <223> OTHER INFORMATION: Synthetic
     30 <220> FEATURE:
     31 <221> NAME/KEY: CDS
     32 <222> LOCATION: (1)..(1575)
     34 <400> SEQUENCE: 1
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     37 1               5                  10                  15
     39 ctg tac aag tcc gga ctc aga tct cga gct caa gct tcg aat tct gca      96
     40 Leu Tyr Lys Ser Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala
     41             20                  25                  30
     43 gtc gac ggt acc acg cgc acc atg ggt gaa aaa ccc ggg acc agg gtc     144
     44 Val Asp Gly Thr Thr Arg Thr Met Gly Glu Lys Pro Gly Thr Arg Val
     45         35                  40                  45
     47 ttc aag aag tcg agc cct aac tgc aag ctc acc gtg tac ttg ggc aag     192
     48 Phe Lys Lys Ser Ser Pro Asn Cys Lys Leu Thr Val Tyr Leu Gly Lys
     49     50                  55                  60
     51 cgt gac ttt gtg gat cac ttg gac aaa gtg gat cct gtc gat ggt gtg     240
     52 Arg Asp Phe Val Asp His Leu Asp Lys Val Asp Pro Val Asp Gly Val
     53 65                  70                  75                  80
     55 gtg ctt gtg gat cct gac tac ttg aag gac cgg aaa gtg ttt gtg acc     288
     56 Val Leu Val Asp Pro Asp Tyr Leu Lys Asp Arg Lys Val Phe Val Thr
     57                 85                  90                  95
     59 ctc acc tgt gcc ttc cgc tat ggc cga gaa gac ctg gat gta ctg ggc     336
     60 Leu Thr Cys Ala Phe Arg Tyr Gly Arg Glu Asp Leu Asp Val Leu Gly
     61             100                 105                 110
     63 ctg tct ttc cgc aaa gat ctg ttc atc gcc acc tac cag gcc ttc ccc     384
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64 Leu Ser Phe Arg Lys Asp Leu Phe Ile Ala Thr Tyr Gln Ala Phe Pro
65         115                 120                 125
67 ccc atg ccc aac cca cct cgg ccc ccc acc cgc cta cag gac cga ctg      432
68 Pro Met Pro Asn Pro Pro Arg Pro Pro Thr Arg Leu Gln Asp Arg Leu
69     130                 135                 140
71 ctg aag aag ttg ggc cag cat gcc cac ccc ttt ttt ttc aca ata ccc      480
72 Leu Lys Lys Leu Gly Gln His Ala His Pro Phe Phe Phe Thr Ile Pro
73 145                 150                 155                 160
75 cag aat ttg cct tgc tcc gtc aca ctg cag cca gga ccg gag gac aca      528
76 Gln Asn Leu Pro Cys Ser Val Thr Leu Gln Pro Gly Pro Glu Asp Thr
77                 165                 170                 175
79 ggg aag gcc tgt gga gta gac ttt gag att cga gcc ttc tgt gcc aaa      576
80 Gly Lys Ala Cys Gly Val Asp Phe Glu Ile Arg Ala Phe Cys Ala Lys
81             180                 185                 190
83 tct ata gaa gaa aaa agc cac aaa agg aac tcc gtg cgg ctt atc atc      624
84 Ser Ile Glu Glu Lys Ser His Lys Arg Asn Ser Val Arg Leu Ile Ile
85         195                 200                 205
87 aga aag gta cag ttt gct cct gag aca ccc ggc ccc cag cca tca gct      672
88 Arg Lys Val Gln Phe Ala Pro Glu Thr Pro Gly Pro Gln Pro Ser Ala
89     210                 215                 220
91 gaa acc aca cgc cac ttc ctc atg tct gac cgg agg tcc ctg cac cta      720
92 Glu Thr Thr Arg His Phe Leu Met Ser Asp Arg Arg Ser Leu His Leu
93 225                 230                 235                 240
95 gag gct tcc ctg gac aaa gag ctg tac tac cat ggg gaa ccc ctc aat      768
96 Glu Ala Ser Leu Asp Lys Glu Leu Tyr Tyr His Gly Glu Pro Leu Asn
97                 245                 250                 255
99 gtc aac gtc cac gtc acc aac aat tct gcc aag acc gtc aag aag atc      816
100 Val Asn Val His Val Thr Asn Asn Ser Ala Lys Thr Val Lys Lys Ile
101             260                 265                 270
103 aga gtg tct gtg aga cag tat gcc gac att tgc ctc ttc agc acc gcg      864
104 Arg Val Ser Val Arg Gln Tyr Ala Asp Ile Cys Leu Phe Ser Thr Ala
105         275                 280                 285
107 cag tac aag tgt cct gtg gct cag ctt gaa caa gat gac cag gtg tct      912
108 Gln Tyr Lys Cys Pro Val Ala Gln Leu Glu Gln Asp Asp Gln Val Ser
109     290                 295                 300
111 ccc agt tcc aca ttc tgc aag gtg tac acc ata acc ccg ctg ctc agt      960
112 Pro Ser Ser Thr Phe Cys Lys Val Tyr Thr Ile Thr Pro Leu Leu Ser
113 305                 310                 315                 320
115 gac aac cca gag aag cgt ggc ctt gcc ctt gat ggg caa ctc aag cac     1008
116 Asp Asn Pro Glu Lys Arg Gly Leu Ala Leu Asp Gly Gln Leu Lys His
117                 325                 330                 335
119 caa gac acc aac ctg gct tcc agc acc att gtg aag gag gga gcc aac     1056
120 Gln Asp Thr Asn Leu Ala Ser Ser Thr Ile Val Lys Glu Gly Ala Asn
121             340                 345                 350
123 aag gag gtg ctg gga atc cta gta tcc tac agg gtc aac gtg aag ctg     1104
124 Lys Glu Val Leu Gly Ile Leu Val Ser Tyr Arg Val Asn Val Lys Leu
125         355                 360                 365
127 gtg gtg tct cca ggc ggc gat gtc tcc gtg gag cta cct ttc gtc cta     1152
128 Val Val Ser Pro Gly Gly Asp Val Ser Val Glu Leu Pro Phe Val Leu
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129     370                 375                 380
131 atg cac ccc aag ccc cac gac cac atc acc ctt ccc cga ccc cag tca     1200
132 Met His Pro Lys Pro His Asp His Ile Thr Leu Pro Arg Pro Gln Ser
133 385                 390                 395                 400
135 gcc ccc cgg gaa ata gac atc cct gtg gat acc aac ctc att gaa ttc     1248
136 Ala Pro Arg Glu Ile Asp Ile Pro Val Asp Thr Asn Leu Ile Glu Phe
137                 405                 410                 415
139 gat acc aac tat gcc aca gac gac gac atc gtg ttt gag gac ttt gcg     1296
140 Asp Thr Asn Tyr Ala Thr Asp Asp Asp Ile Val Phe Glu Asp Phe Ala
141             420                 425                 430
143 agg ctt cgg ctg aag ggg atg aag gat gac gac tgt gat gac cag ttc     1344
144 Arg Leu Arg Leu Lys Gly Met Lys Asp Asp Asp Cys Asp Asp Gln Phe
145         435                 440                 445
147 tgc gtc gac cag atc ttc gtg aag act ctg act ggt aag acc atc acc     1392
148 Cys Val Asp Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
149     450                 455                 460
151 ctc gag gtg gag ccc agt gac acc atc gag aat gtc aag gca aag atc     1440
152 Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile
153 465                 470                 475                 480
155 caa gat aag gaa ggc att cct cct gat cag cag agg ttg atc ttt gcc     1488
156 Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
157                 485                 490                 495
159 gga aaa cag ctg gaa gat ggt cgt acc ctg tct gac tac aac atc cag     1536
160 Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln
161             500                 505                 510
163 aaa gag tcc acc ttg cac ctg gta ctc cgt ctc aga ggt gggtga         1581
164 Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly
165         515                 520                 525
168 <210> SEQ ID NO: 2
169 <211> LENGTH: 525
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Synthetic Construct
176 <400> SEQUENCE: 2
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183             20                  25                  30
186 Val Asp Gly Thr Thr Arg Thr Met Gly Glu Lys Pro Gly Thr Arg Val
187         35                  40                  45
190 Phe Lys Lys Ser Ser Pro Asn Cys Lys Leu Thr Val Tyr Leu Gly Lys
191     50                  55                  60
194 Arg Asp Phe Val Asp His Leu Asp Lys Val Asp Pro Val Asp Gly Val
195 65                  70                  75                  80
198 Val Leu Val Asp Pro Asp Tyr Leu Lys Asp Arg Lys Val Phe Val Thr
199                 85                  90                  95
202 Leu Thr Cys Ala Phe Arg Tyr Gly Arg Glu Asp Leu Asp Val Leu Gly
203             100                 105                 110
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206 Leu Ser Phe Arg Lys Asp Leu Phe Ile Ala Thr Tyr Gln Ala Phe Pro
207         115                 120                 125
210 Pro Met Pro Asn Pro Pro Arg Pro Pro Thr Arg Leu Gln Asp Arg Leu
211     130                 135                 140
214 Leu Lys Lys Leu Gly Gln His Ala His Pro Phe Phe Phe Thr Ile Pro
215 145                 150                 155                 160
218 Gln Asn Leu Pro Cys Ser Val Thr Leu Gln Pro Gly Pro Glu Asp Thr
219                 165                 170                 175
222 Gly Lys Ala Cys Gly Val Asp Phe Glu Ile Arg Ala Phe Cys Ala Lys
223             180                 185                 190
226 Ser Ile Glu Glu Lys Ser His Lys Arg Asn Ser Val Arg Leu Ile Ile
227         195                 200                 205
230 Arg Lys Val Gln Phe Ala Pro Glu Thr Pro Gly Pro Gln Pro Ser Ala
231     210                 215                 220
234 Glu Thr Thr Arg His Phe Leu Met Ser Asp Arg Arg Ser Leu His Leu
235 225                 230                 235                 240
238 Glu Ala Ser Leu Asp Lys Glu Leu Tyr Tyr His Gly Glu Pro Leu Asn
239                 245                 250                 255
242 Val Asn Val His Val Thr Asn Asn Ser Ala Lys Thr Val Lys Lys Ile
243             260                 265                 270
246 Arg Val Ser Val Arg Gln Tyr Ala Asp Ile Cys Leu Phe Ser Thr Ala
247         275                 280                 285
250 Gln Tyr Lys Cys Pro Val Ala Gln Leu Glu Gln Asp Asp Gln Val Ser
251     290                 295                 300
254 Pro Ser Ser Thr Phe Cys Lys Val Tyr Thr Ile Thr Pro Leu Leu Ser
255 305                 310                 315                 320
258 Asp Asn Pro Glu Lys Arg Gly Leu Ala Leu Asp Gly Gln Leu Lys His
259                 325                 330                 335
262 Gln Asp Thr Asn Leu Ala Ser Ser Thr Ile Val Lys Glu Gly Ala Asn
263             340                 345                 350
266 Lys Glu Val Leu Gly Ile Leu Val Ser Tyr Arg Val Asn Val Lys Leu
267         355                 360                 365
270 Val Val Ser Pro Gly Gly Asp Val Ser Val Glu Leu Pro Phe Val Leu
271     370                 375                 380
274 Met His Pro Lys Pro His Asp His Ile Thr Leu Pro Arg Pro Gln Ser
275 385                 390                 395                 400
278 Ala Pro Arg Glu Ile Asp Ile Pro Val Asp Thr Asn Leu Ile Glu Phe
279                 405                 410                 415
282 Asp Thr Asn Tyr Ala Thr Asp Asp Asp Ile Val Phe Glu Asp Phe Ala
283             420                 425                 430
286 Arg Leu Arg Leu Lys Gly Met Lys Asp Asp Asp Cys Asp Asp Gln Phe
287         435                 440                 445
290 Cys Val Asp Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
291     450                 455                 460
294 Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile
295 465                 470                 475                 480
298 Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
299                 485                 490                 495
302 Gly Lys Gln Leu Glu Asp Gly Arg Thr Leu Ser Asp Tyr Asn Ile Gln
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303             500                 505                 510
306 Lys Glu Ser Thr Leu His Leu Val Leu Arg Leu Arg Gly
307         515                 520                 525
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311 <211> LENGTH: 1581
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Synthetic
319 <220> FEATURE:
320 <221> NAME/KEY: CDS
321 <222> LOCATION: (1)..(1581)
323 <400> SEQUENCE: 3
324 ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag       48
325 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
326 1               5                   10                  15
328 ctg tac aag tcc gga ctc aga tct cga gct caa gct tcg aat tct gca       96
329 Leu Tyr Lys Ser Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala
330             20                  25                  30
332 gtc gac ggt acc acg cgc acc atg ggt gaa aaa ccc ggg acc agg gtc      144
333 Val Asp Gly Thr Thr Arg Thr Met Gly Glu Lys Pro Gly Thr Arg Val
334         35                  40                  45
336 ttc aag aag tcg agc cct aac tgc aag ctc acc gtg tac ttg ggc aag      192
337 Phe Lys Lys Ser Ser Pro Asn Cys Lys Leu Thr Val Tyr Leu Gly Lys
338     50                  55                  60
340 cgt gac ttt gtg gat cac ttg gac aaa gtg gat cct gtc gat ggt gtg      240
341 Arg Asp Phe Val Asp His Leu Asp Lys Val Asp Pro Val Asp Gly Val
342 65                  70                  75                  80
344 gtg ctt gtg gat cct gac tac ttg aag gac cgg aaa gtg ttt gtg acc      288
345 Val Leu Val Asp Pro Asp Tyr Leu Lys Asp Arg Lys Val Phe Val Thr
346                 85                  90                  95
348 ctc acc tgt gcc ttc cgc tat ggc cga gaa gac ctg gat gta ctg ggc      336
349 Leu Thr Cys Ala Phe Arg Tyr Gly Arg Glu Asp Leu Asp Val Leu Gly
350             100                 105                 110
352 ctg tct ttc cgc aaa gat ctg ttc atc gcc acc tac cag gcc ttc ccc      384
353 Leu Ser Phe Arg Lys Asp Leu Phe Ile Ala Thr Tyr Gln Ala Phe Pro
354         115                 120                 125
356 ccc atg ccc aac cca cct cgg ccc ccc acc cgc cta cag gac cga ctg      432
357 Pro Met Pro Asn Pro Pro Arg Pro Pro Thr Arg Leu Gln Asp Arg Leu
358     130                 135                 140
360 ctg aag aag ttg ggc cag cat gcc cac ccc ttt ttt ttc aca ata ccc      480
361 Leu Lys Lys Leu Gly Gln His Ala His Pro Phe Phe Phe Thr Ile Pro
362 145                 150                 155                 160
364 cag aat ttg cct tgc tcc gtc aca ctg cag cca gca ccg gag gac aca      528
365 Gln Asn Leu Pro Cys Ser Val Thr Leu Gln Pro Ala Pro Glu Asp Thr
366                 165                 170                 175
368 ggg aag gcc tgt gga gta gac ttt gag att cga gcc ttc tgt gcc aaa      576
369 Gly Lys Ala Cys Gly Val Asp Phe Glu Ile Arg Ala Phe Cys Ala Lys
370             180                 185                 190
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/14/2006
PATENT APPLICATION: **US/10/543,122** TIME: 10:29:11

Input Set : **A:\186563-US-2.ST25.txt**
Output Set: **N:\CRF4\06142006\J543122.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6

VERIFICATION SUMMARY DATE: 06/14/2006
PATENT APPLICATION: **US/10/543,122** TIME: 10:29:11

Input Set : **A:\186563-US-2.ST25.txt**
Output Set: **N:\CRF4\06142006\J543122.raw**

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date